

H		gagtctaacacggaccaaggagttttaac
M	-60	tgaaaagatagaataaatggcctcgtgc
H		M E W P A R L C G
		ATGGAGTGGCCGGCGCGGCTCTGCGGGC
		* * * *
M	1	ATGGCGCGGCCAGCGCTGCTGGGCGAGC
M	1	M A R P A L L G E
H		G G G G A P T E T
H		GGGGGCGGGGGCGCGCCTACGGAAACTC
		* * * *
M	61	GGCCAAGTTGCCGCGGCCACAGAAGTTC
M	21	G Q V A A A T E V
H		E N L C T V I W T
H		GAAAACCTCTGCACAGTAATATGGACAT
		* * * * * * *
M	121	GAAAATCTCTGCACGATAATATGGACGT
M	41	E N L C T I I W T
H		S L W Y F S H F G
H		AGTCTATGGTATTTTAGTCATTTTGGCG
		* * * * *
M	181	ACTCTCAGATATTTTAGTCACTTTGATG
M	61	T L R Y F S H F D

Fig. 7A

acgtgcgggccggggttccgagggcgagaggctgc

.....

cgaattcgggcacgagccgagggcgaggggcctgc

L W A L L L C A G G G G
TGTGGGCGCTGCTGCTCTGCGCCGGCGGGGGGC

* * *

TGTTGGTGCTGCTACTGTGGACCGCCACCGTG---

L L V L L L W T A T V -

Q P P V T N L S V S V

AGCCACCTGTGACAAATTTGAGTGTCTCTGTT

* * * * *

AGCCACCTGTGACGAATTTGAGCGTCTCTGTC

Q P P V T N L S V S V

W N P P E G A S S N C

GGAATCCACCCGAGGGAGCCAGCTCAAATTGT

* * * * *

GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC

W S P P E G A S P N C

D K Q D K K I A P E T

ACAAACAAGATAAGAAAATAGCTCCGGAAACT

* * * * *

ACCAACAGGATAAGAAAATTGCTCCAGAAACT

D Q Q D K K I A P E T

Fig. 7B

H		R	R	S	I	E	V	P	L	N																						
H		C	G	T	C	G	T	T	C	A	T	A	G	A	G	T	A	C	C	C	T	G	A	A	T	G						
		*				*			*		*		*		*		*		*		*		*		*							
M	241	C	A	T	C	G	T	A	A	A	G	A	G	A	A	T	T	A	C	C	C	C	T	G	G	A	T	G				
M	81	H	R	K	E	E	L	P	L	D																						
H		S	T	N	E	S	E	K	P	S																						
H		A	G	C	A	C	A	A	T	G	A	G	A	G	T	G	A	G	A	A	G	C	C	T	A	G	C	A				
		*		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*				
M	301	A	G	T	G	C	C	A	A	T	G	A	A	A	G	T	G	A	G	A	A	G	C	C	T	A	G	C				
M	101	S	A	N	E	S	E	K	P	S																						
H		G	D	P	E	S	A	V	T	E																						
H		G	G	T	G	A	T	C	C	T	G	A	G	T	C	T	G	C	T	G	T	G	A	C	T	G	A	A	C			
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*				
M	361	G	G	T	G	A	T	C	C	T	G	A	G	T	C	C	G	C	T	G	T	G	A	C	T	G	A	G	C			
M	121	G	D	P	E	S	A	V	T	E																						
H		K	C	S	W	L	P	G	R	N																						
H		A	A	G	T	G	T	T	C	T	T	G	G	C	T	C	C	C	T	G	G	A	A	G	G	A	A	T	A			
		*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*				
M	421	A	A	G	T	G	T	T	C	C	T	T	G	G	C	T	C	C	C	T	G	G	A	A	G	G	A	A	T	A		
M	141	K	C	S	W	L	P	G	R	N																						
H		W	H	R	S	L	E	K	I	H																						
H		T	G	G	C	A	C	A	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	T	T	C	A	T	C

Fig.7C

E R I C L Q V G S Q C
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
* * * * *
AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
E K I C L Q V G S Q C

I L V E K C I S P P E
TTTTGGTTGAAAAATGCATCTCACCCCCAGAA
* * * * *
CTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
P L V K K C I S P P E

L Q C I W H N L S Y M
TTCAATGCATTTGGCACAACCTGAGCTACATG
* * * * *
TCAAGTGCATTTGGCATAACCTGAGCTATATG
L K C I W H N L S Y M

T S P D T N Y T L Y Y
CCAGTCCCGACACTAATACTCTCTACTAT
* * * * *
CAAGCCCTGACACACACTATACTCTGTACTAT
T S P D T H Y T L Y Y

Q C E N I F R E G Q Y
AATGTGAAAACATCTTTAGAGAAGGCCAATAC

Fig. 7D

			*		*	*	*	*	
M	481		TGGTACAGCAGCCTGGAGAAAAGTCGTC						
M	161		W Y S S L E K S R						
H			F G C S F D L T K						
H			TTTGGTTGTTTCCTTTGATCTGACCAAAG						
				*	*	*		*	*
M	541		ATTGCTTGTTTCCTTTAAATTGACTAAAG						
M	181		I A C S F K L T K						
H			Q I M V K D N A G						
H			CAAATAATGGTCAAGGATAATGCAGGAA						
				*	*	*	*	*	*
M	598 601		CAAATAATGGTCAAGGATAATGCTGGGA						
M	201 200		Q I M V K D N A G						
H			T S R V K P D P P						
H			ACTTCCCGTGTGAAACCTGATCCTCCAC						
				*	*		*	*	*
M	658 661		ACTTCCTATGTGAAACCTGATCCTCCAC						
M	221 220		T S Y V K P D P P						
H			L Y V Q W E N P Q						
H			CTATATGTGCAATGGGAGAATCCACAGA						
				*	*	*	*	*	*
M	718 721		TTATTAGTGCAGTGGAAGAATCCACAAA						
M	241 240		L L V Q W K N P Q						

Fig. 7E

* * * * * * * *
AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q C E N I Y R E G Q H
V K D S S F E Q H S V
TGAAGGATTCCAGTTTGAACAACACAGTGTC
* * * * *
TGGAACCT - - - AGTTTTGAACATCAGAACG TT
V E P - S F E H Q N V
K I K P S F N I V P L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
* * * * *
AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
K I R P S C K I V S L
H I K N L S F H N D D
ATATTAAAAACCTCTCCTTCCACAATGATGAC
* * * * *
ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H I K H L L L K N G A
N F I S R C L F Y E V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
* * * * *
ATTTTAGAAGCAGATGCTTAACCTTATGAAGTG
N F R S R C L T Y E V

Fig. 7F

H		E	V	N	N	S	Q	T	E	T
H		GAAGTCAATAACAGCCAAACTGAGACAC								
	778	*	*	*	*	*	*			
M	781	GAGGTCAATAATACTCAAACCGACCGAC								
M	261 260	E	V	N	N	T	Q	T	D	R
H		E	N	P	E	F	E	R	N	V
H		GAGAATCCAGAATTTGAGAGAAATGTGG								
	838	*		*		*	*			
M	841	CAGAATTCCGAATCTGATAGAAACATGG								
M	281 280	Q	N	S	E	S	D	R	N	M
H		L	P	D	T	L	N	T	V	R
H		CTTCCTGATACTTTGAACACAGTCAGAA								
	898	*		*		*	*	*		
M	901	CTTGCCCGACGCTGTCTACACAGTCAGAG								
M	301 300	L	A	D	A	V	Y	T	V	R
H		D	D	K	L	W	S	N	W	S
H		GATGACAAACTCTGGAGTAATTGGAGCC								
	958	*	*	*	*	*	*	*	*	
M	961	GACAACAAACTGTGGAGTGATTGGAGTG								
M	321 320	D	N	K	L	W	S	D	W	S
H		T	L	Y	I	T	M	L	L	I
H		AACTCTACATAACCATGTTACTCATTG								

Fig. 7G

H N V F Y V Q E A K C
ATAATGTTTTCTACGTCCAAGAGGCTAAATGT

* * * * *

ATAATATTTTAGAGGTTGAAGAGGACAAATGC

H N I L E V E E D K C

E N T S C F M V P G V
AGAATACATCTTGTTTCATGGTCCCTGGTGTT

* * * * *

AGGGTACAAGTTGTTTCCAACCTCCCTGGTGTT

E G T S C F Q L P G V

I R V K T N K L C Y E
TAAGAGTCAAAACAAATAAGTTATGCTATGAG

* * * * *

TAAGAGTCAAAACAAACAAGTTATGCTTTGAT

V R V K T N K L C F D

Q E M S I G K K R N S
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC

* * * * *

AAGCACAGAGTATAGGTAAGGAGCAAAACTCC

E A Q S I G K E Q N S

V P V I V A G A I I V

TTCCAGTCATCGTCGCAGGTGCAATCATAGTA

Fig. 7H

			*		*		*	*	*	*	
M	1021	1018	ACCTTCTACACCACCATGTTACTCACCA								
M	341	340	T F Y T T M L L T								
H			L L L Y L K R L K								
H			CTCCTGCTTTACCTAAAAAGGCTCAAGA								
				*	*		*	*	*	*	*
M	1081	1078	CTCCTTTTTTACCTGAAAAGGCTTAAGA								
M	361	360	L L F Y L K R L K								
H			K I F K E M F G D								
H			AAGATTTTTTAAAGAAATGTTTGGAGACC								
				*	*	*	*	*	*	*	*
M	1141	1138	AAGATTTTTTAAAGAAATGTTTGGAGACC								
M	381	380	K I F K E M F G D								
H			D I Y E K Q T K E								
H			GACATCTATGAGAAGCAAACCAAGGAGG								
				*	*	*	*	*	*	*	*
M	1201	1198	GACATCTATGAGAAACAATCCAAAGAAG								
M	401	400	D I Y E K Q S K E								
H			K K A S Q *								
H			AAGAAAGCCTCTCAGTGatggagataat								
				*	*	*					
M	1261	1258	AAGAAAGCAGCTCCTTGatgggggagaag								
M	421	420	K K A A P *								

Fig. 7I

* * * * *

TTCCAGTCTTTGTCGCAGTGGCAGTCATAATC
I P V F V A V A V I I

I I I F P P I P D P G
TTATTATATTCCCTCCAATTCCTGATCCTGGC
* * * * *

TCATTATATTTCCCTCCAATTCCTGATCCTGGC
I I I F P P I P D P G

Q N D D T L H W K K Y
AGAATGATGATACTCTGCACTGGAAGAAGTAC
* * * * *

AGAATGATGATACCCTGCACTGGAAGAAGTAT
Q N D D T L H W K K Y

E T D S V V L I E N L
AAACCGACTCTGTAGTGCTGATAGAAAACCTG
* * * * *

AAACGGATTCTGTAGTGCTGATAGAAAACCTG
E T D S V V L I E N L

ttatTTTTaccttcactgtgaccttgagaaga
tgatttctttcttgccttcaatgtgaccctgt

Fig. 7J